



In the Sequence Listing:

Please insert the attached paper copy of the Sequence Listing as new pages 1-27 in the above-captioned application. A computer-readable copy (CRF copy) of the Sequence Listing accompanies this response.

**AMENDMENTS**

Please replace the paragraph beginning at page 6, line 19, with the following rewritten paragraph:

A2  
--Figure 3A-3B depicts an alignment of the protein kinase domain of human 32374 with a consensus amino acid sequence derived from a hidden Markov model (HMM) from PFAM. The upper sequence is the consensus amino acid sequence (SEQ ID NO:7), while the lower amino acid sequence corresponds to amino acids 1 to 231 of SEQ ID NO:2.--

Please replace the paragraph beginning at page 8, line 12, with the following rewritten paragraph:

A3  
--Figure 12A-12B depicts a BLAST alignment of human 32374 with a consensus amino acid sequence derived from a ProDomain "Kinase kinase-related serine/threonine serine/threonine-protein" (Release 2001.1; <http://www.toulouse.inra.fr/prodom.html>). The lower sequence is amino acid residues 82 to 296 of the 542 amino acid consensus sequence (SEQ ID NO:16), while the upper amino acid sequence corresponds to the "Kinase kinase-related serine/threonine serine/threonine-protein" domain of human 32374, amino acid residues 29 to 262 of SEQ ID NO:2.--

Please replace the paragraph beginning at page 8, line 19, with the following rewritten paragraph:

A4  
--Figure 13A-13E depicts a cDNA sequence (SEQ ID NO:4) and predicted amino acid sequence (SEQ ID NO:5) of human 18431. The methionine-initiated open reading frame of human 18431 (without the 5' and 3' untranslated regions) extends from nucleotide position 1 to position 2682 of SEQ ID NO:6, not including the terminal codon.--